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# /usr/local/lexicon/bin/fasta34 -Q /tmp/fasta3.Mlaab5 /tmp/fasta3.Nlaab5
FASTA searches a protein or DNA sequence data bank
version 3.4t25 Nov 12, 2004
```

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
Query library /tmp/fasta3.Mlaab5 vs /tmp/fasta3.Nlaab5 library
searching /tmp/fasta3.Nlaab5 library
```

```
1>>>FIRST_SEQUENCE - 3222 nt
vs /tmp/fasta3.Nlaab5 library
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6109 residues in      1 sequences
Altschul/Gish params: n0: 3222 Lambda: 0.192 K: 0.177 H: 0.360
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FASTA (3.47 Mar 2004) function [optimized, +5/-4 matrix (5:-4)] ktup: 6
join: 85, opt: 70, open/ext: -12/-4, width: 16
Scan time: 0.030
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```
The best scores are:                                opt bits E(1)
gi|24234740|ref|NM_153618.1| Homo sapiens sema (6109) [f] 16101 4462.5      0
gi|24234740|ref|NM_153618.1| Homo sapiens sema (6109) [r]   76 23.6      0.79
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>>gi|24234740|ref|NM_153618.1| Homo sapiens sema domain, (6109 nt)
initn: 16101 init1: 16101 opt: 16101 Z-score: 24031.7 bits: 4462.5 E(): 0
banded Smith-Waterman score: 16101; 99.969% identity (99.969% similar) in 3222 nt o
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                                10      20      30
FIRST_      ATGAGGGTCTTCCTGCTTTGTGCCTACATA
              :
gi|242      GGGGCCACCCCTGACTTCACCTTGGCCCAACCATGAGGGTCTTCCTGCTTTGTGCCTACATA
      410      420      430      440      450      460
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                                40      50      60      70      80      90
FIRST_      CTGCTGCTGATGGTTTCCCAGTTGAGGGCAGTCAGCTTTCCTGAAGATGATGAACCCCTT
              :
gi|242      CTGCTGCTGATGGTTTCCCAGTTGAGGGCAGTCAGCTTTCCTGAAGATGATGAACCCCTT
      470      480      490      500      510      520
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                                100     110     120     130     140     150
FIRST_      AATACTGTCTGACTATCACTATTCAAGGCAATATCCGGTTTTTTAGAGGACGCCCTTCAGGC
              :
gi|242      AATACTGTCTGACTATCACTATTCAAGGCAATATCCGGTTTTTTAGAGGACGCCCTTCAGGC
      530      540      550      560      570      580
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                                160     170     180     190     200     210
FIRST_      AATGAATCGCAGCACAGGCTGGACTTTCAGCTGATGTTGAAAATTCGAGACACACTTTAT
              :
gi|242      AATGAATCGCAGCACAGGCTGGACTTTCAGCTGATGTTGAAAATTCGAGACACACTTTAT
      590      600      610      620      630      640
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                                220     230     240     250     260     270
FIRST_      ATTGCTGGCAGGGATCAAGTTTATACAGTAACTTAAATGAAATGCCCAAACAGAAGTA
              :
gi|242      ATTGCTGGCAGGGATCAAGTTTATACAGTAACTTAAATGAAATGCCCAAACAGAAGTA
      650      660      670      680      690      700
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                                280     290     300     310     320     330
FIRST_      ATACCCAACAAGAACTGACATGGCGATCAAGACAACAGGATCGAGAAAACGTGTGCTATG
              :
gi|242      ATACCCAACAAGAACTGACATGGCGATCAAGACAACAGGATCGAGAAAACGTGTGCTATG
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      710      720      730      740      750      760
FIRST_      340      350      360      370      380      390
AAAGGCAAGCATAAAGATGAATGCCACAACCTTTATCAAAGTATTTGTTCCAAGAAACGAT
gi|242      770      780      790      800      810      820
AAAGGCAAGCATAAAGATGAATGCCACAACCTTTATCAAAGTATTTGTTCCAAGAAACGAT

      400      410      420      430      440      450
FIRST_      GAGATGGTTTTTTGTTTGTGGTACCAATGCATTCAATCCCATGTGTAGATACTACAGGTTG
gi|242      830      840      850      860      870      880
GAGATGGTTTTTTGTTTGTGGTACCAATGCATTCAATCCCATGTGTAGATACTACAGGTTG

      460      470      480      490      500      510
FIRST_      AGTACCTTAGAATATGATGGGGAAGAAATTAGTGGCCTGGCAAGATGCCCATTTGATGCC
gi|242      890      900      910      920      930      940
AGTACCTTAGAATATGATGGGGAAGAAATTAGTGGCCTGGCAAGATGCCCATTTGATGCC

      520      530      540      550      560      570
FIRST_      AGACAAACCAATGTTGCCCTCTTTGCTGATGGGAAGCTGTATTCTGCCACAGTGGCTGAC
gi|242      950      960      970      980      990      1000
AGACAAACCAATGTTGCCCTCTTTGCTGATGGGAAGCTGTATTCTGCCACAGTGGCTGAC

      580      590      600      610      620      630
FIRST_      TTCTTGGCCAGCGATGCCGTTATTTATCGAAGCATGGGTGATGGATCTGCCCTTCGCACA
gi|242      1010      1020      1030      1040      1050      1060
TTCTTGGCCAGCGATGCCGTTATTTATCGAAGCATGGGTGATGGATCTGCCCTTCGCACA

      640      650      660      670      680      690
FIRST_      ATAAAATATGATTCCAAATGGATAAAAGAGCCACACTTTCTTCATGCCATAGAATATGGA
gi|242      1070      1080      1090      1100      1110      1120
ATAAAATATGATTCCAAATGGATAAAAGAGCCACACTTTCTTCATGCCATAGAATATGGA

      700      710      720      730      740      750
FIRST_      AACTATGTCTATTTCTTCTTTTCGAGAAATCGCTGTCTGAACATAATAATTTAGGCAAGGCT
gi|242      1130      1140      1150      1160      1170      1180
AACTATGTCTATTTCTTCTTTTCGAGAAATCGCTGTCTGAACATAATAATTTAGGCAAGGCT

      760      770      780      790      800      810
FIRST_      GTGTATTCCC CGTGGCCCGCATATGTAAAAACGACATGGGTGGTTC CAGCGGGTCCTG
gi|242      1190      1200      1210      1220      1230      1240
GTGTATTCCC CGTGGCCCGCATATGTAAAAACGACATGGGTGGTTC CAGCGGGTCCTG

      820      830      840      850      860      870
FIRST_      GAGAAACACTGGACTTCATTTCTAAAGGCTCGGCTGAACTGTTCTGTCCCTGGAGATTCTG
gi|242      1250      1260      1270      1280      1290      1300
GAGAAACACTGGACTTCATTTCTAAAGGCTCGGCTGAACTGTTCTGTCCCTGGAGATTCTG

      880      890      900      910      920      930
FIRST_      TTTTTCTACTTTGATGTTCTGCAGTCTATTACAGACATAATACAAATCAATGGCATCCCC
gi|242      TTTTTCTACTTTGATGTTCTGCAGTCTATTACAGACATAATACAAATCAATGGCATCCCC
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1310      1320      1330      1340      1350      1360
FIRST_      940      950      960      970      980      990
FIRST_ ACTGTGGTCGGGGTGTTTACCACGCAGCTCAATAGCATCCCTGGTTCTGCTGTCTGTGCA
      .....
gi|242 ACTGTGGTCGGGGTGTTTACCACGCAGCTCAATAGCATCCCTGGTTCTGCTGTCTGTGCA
      1370      1380      1390      1400      1410      1420

      1000      1010      1020      1030      1040      1050
FIRST_ TTTAGCATGGATGACATTGAAAAAGTATTCAAAGGACGGTTTAAGGAACAGAAAACCTCCA
      .....
gi|242 TTTAGCATGGATGACATTGAAAAAGTATTCAAAGGACGGTTTAAGGAACAGAAAACCTCCA
      1430      1440      1450      1460      1470      1480

      1060      1070      1080      1090      1100      1110
FIRST_ GATTCTGTTTGGACAGCAGTTCCCGAAGACAAAGTGCCAAAGCCAAGGCCTGGCTGTTGT
      .....
gi|242 GATTCTGTTTGGACAGCAGTTCCCGAAGACAAAGTGCCAAAGCCAAGGCCTGGCTGTTGT
      1490      1500      1510      1520      1530      1540

      1120      1130      1140      1150      1160      1170
FIRST_ GCAAAACACGGCCTTGCCGAAGCTTATAAAACCTCCATCGATTTCCTCGGATGAAACTCTG
      .....
gi|242 GCAAAACACGGCCTTGCCGAAGCTTATAAAACCTCCATCGATTTCCTCGGATGAAACTCTG
      1550      1560      1570      1580      1590      1600

      1180      1190      1200      1210      1220      1230
FIRST_ TCATTTCATCAAATCTCATCCCTGATGGACTCTGCCGTTCCACCCATTGCCGATGAGCCC
      .....
gi|242 TCATTTCATCAAATCTCATCCCTGATGGACTCTGCCGTTCCACCCATTGCCGATGAGCCC
      1610      1620      1630      1640      1650      1660

      1240      1250      1260      1270      1280      1290
FIRST_ TGGTTCACAAAGACTCGGGTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTTCAGCC
      .....
gi|242 TGGTTCACAAAGACTCGGGTCAGGTACAGACTGACGGCCATCTCAGTGGACCATTTCAGCC
      1670      1680      1690      1700      1710      1720

      1300      1310      1320      1330      1340      1350
FIRST_ GGACCCCTACCAGAACTACACAGTCATCTTTGTTGGCTCTGAAGCTGGCATGGTACTTAAA
      .....
gi|242 GGACCCCTACCAGAACTACACAGTCATCTTTGTTGGCTCTGAAGCTGGCATGGTACTTAAA
      1730      1740      1750      1760      1770      1780

      1360      1370      1380      1390      1400      1410
FIRST_ GTTCTGGCAAAGACCAGTCCTTTCTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAA
      .....
gi|242 GTTCTGGCAAAGACCAGTCCTTTCTCTTTGAACGACAGCGTATTACTGGAAGAGATTGAA
      1790      1800      1810      1820      1830      1840

      1420      1430      1440      1450      1460      1470
FIRST_ GCCTACAACCATGCAAAGTGCAAGTGCTGAGAATGAGGAAGACAAAAAGGTCATCTCATTA
      .....
gi|242 GCCTACAACCATGCAAAGTGCAAGTGCTGAGAATGAGGAAGACAAAAAGGTCATCTCATTA
      1850      1860      1870      1880      1890      1900

      1480      1490      1500      1510      1520      1530
FIRST_ CAGTTGGATAAAGATCACCACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATC
      .....
gi|242 CAGTTGGATAAAGATCACCACGCTTTATATGTGGCGTTCTCTAGCTGCATTATCCGCATC
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1910      1920      1930      1940      1950      1960
FIRST_      1540      1550      1560      1570      1580      1590
FIRST_ CCCCTCAGTCGCTGTGAGCGTTATGGATCATGTAAAAAGTCTTGTATTGCATCTCGTGAC
      .....
gi|242 CCCCTCAGTCGCTGTGAGCGTTATGGATCATGTAAAAAGTCTTGTATTGCATCTCGTGAC
      1970      1980      1990      2000      2010      2020

      1600      1610      1620      1630      1640      1650
FIRST_ CCGTATTGTGGCTGGTTAAGCCAGGGATCCTGTGGTAGAGTGACCCAGGGATGCTTGCT
      .....
gi|242 CCGTATTGTGGCTGGTTAAGCCAGGGATCCTGTGGTAGAGTGACCCAGGGATGCTTGCT
      2030      2040      2050      2060      2070      2080

      1660      1670      1680      1690      1700      1710
FIRST_ GAAGGATATGAACAAGACACAGAATTCGGCAACACAGCTCATCTAGGGGACTGCCATGAA
      .....
gi|242 GAAGGATATGAACAAGACACAGAATTCGGCAACACAGCTCATCTAGGGGACTGCCATGAA
      2090      2100      2110      2120      2130      2140

      1720      1730      1740      1750      1760      1770
FIRST_ ATTTTGCCTACTTCAACTACACCAGATTACAAAATATTTGGCGGTCCAACATCTGACATG
      .....
gi|242 ATTTTGCCTACTTCAACTACACCAGATTACAAAATATTTGGCGGTCCAACATCTGACATG
      2150      2160      2170      2180      2190      2200

      1780      1790      1800      1810      1820      1830
FIRST_ GAGGTATCTTCATCTTCTGTTACCACAATGGCAAGTATCCCAGAAATCACACCTAAAGTG
      .....
gi|242 GAGGTATCTTCATCTTCTGTTACCACAATGGCAAGTATCCCAGAAATCACACCTAAAGTG
      2210      2220      2230      2240      2250      2260

      1840      1850      1860      1870      1880      1890
FIRST_ ATTGATACCTGGAGACCTAAACTGACAAGCTCTCGGAAATTTGTAGTTCAAGATGATCCA
      .....
gi|242 ATTGATACCTGGAGACCTAAACTGACAAGCTCTCGGAAATTTGTAGTTCAAGATGATCCA
      2270      2280      2290      2300      2310      2320

      1900      1910      1920      1930      1940      1950
FIRST_ AACACTTCTGATTTTACTGATCCTTTATCGGGTATCCCAAAGGGTGACGATGGGAAGTC
      .....
gi|242 AACACTTCTGATTTTACTGATCCTTTATCGGGTATCCCAAAGGGTGACGATGGGAAGTC
      2330      2340      2350      2360      2370      2380

      1960      1970      1980      1990      2000      2010
FIRST_ CAGTCTGGAGAGTCCAACCAGATGGTCCACATGAATGTCCTCATCACCTGTGTCTTTGCT
      .....
gi|242 CAGTCTGGAGAGTCCAACCAGATGGTCCACATGAATGTCCTCATCACCTGTGTCTTTGCT
      2390      2400      2410      2420      2430      2440

      2020      2030      2040      2050      2060      2070
FIRST_ GCTTTTGTTTTGGGGGCATTTCATTGCAGGTGTGGCAGTATACTGCTATCGAGACATGTTT
      .....
gi|242 GCTTTTGTTTTGGGGGCATTTCATTGCAGGTGTGGCAGTATACTGCTATCGAGACATGTTT
      2450      2460      2470      2480      2490      2500

      2080      2090      2100      2110      2120      2130
FIRST_ GTTCGGAACAAACAGAAAGATCCATAAAGATGCAGAGTCCGCCCAGTCATGCACAGACTCC
      .....
gi|242 GTTCGGAACAAACAGAAAGATCCATAAAGATGCAGAGTCCGCCCAGTCATGCACAGACTCC
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2510      2520      2530      2540      2550      2560
FIRST_      2140      2150      2160      2170      2180      2190
FIRST_ AGTGGAAGTTTTGCCAACTGAATGGTCTCTTTGACAGCCCTGTCAAGGAATACCAACAG
gi|242 AGTGGAAGTTTTGCCAACTGAATGGTCTCTTTGACAGCCCTGTCAAGGAATACCAACAG
2570      2580      2590      2600      2610      2620
FIRST_      2200      2210      2220      2230      2240      2250
FIRST_ AATATTGATTCTCCTAAACTGTATAGTAACCTGCTAACCAGTCGGAAAGAGCTACCACCC
gi|242 AATATTGATTCTCCTAAACTGTATAGTAACCTGCTAACCAGTCGGAAAGAGCTACCACCC
2630      2640      2650      2660      2670      2680
FIRST_      2260      2270      2280      2290      2300      2310
FIRST_ AATGGAGATACTAAATCCATGGTAATGGACCATCGAGGGCAACCTCCAGAGTTGGCTGCT
gi|242 AATGGAGATACTAAATCCATGGTAATGGACCATCGAGGGCAACCTCCAGAGTTGGCTGCT
2690      2700      2710      2720      2730      2740
FIRST_      2320      2330      2340      2350      2360      2370
FIRST_ CTTCCCACTCCTGAGTCTACACCCGTGCTTCACCAGAAGACCCTGCAGGCCATGAAGAGC
gi|242 CTTCCCACTCCTGAGTCTACACCCGTGCTTCACCAGAAGACCCTGCAGGCCATGAAGAGC
2750      2760      2770      2780      2790      2800
FIRST_      2380      2390      2400      2410      2420      2430
FIRST_ CACTCAGAAAAGGCCCATGGCCATGGAGCTTCAAGGAAAGAAACCCCTCAGTTTTTTCCG
gi|242 CACTCAGAAAAGGCCCATGGCCATGGAGCTTCAAGGAAAGAAACCCCTCAGTTTTTTCCG
2810      2820      2830      2840      2850      2860
FIRST_      2440      2450      2460      2470      2480      2490
FIRST_ TCTAGTCCGCCACCTCATTCCCCATTAAGTCATGGGCATATCCCCAGTGCCATTGTTCTT
gi|242 TCTAGTCCGCCACCTCATTCCCCATTAAGTCATGGGCATATCCCCAGTGCCATTGTTCTT
2870      2880      2890      2900      2910      2920
FIRST_      2500      2510      2520      2530      2540      2550
FIRST_ CCAAATGCTACCCATGACTACAACACGTCTTTCTCAAACCTCCAATGCTCACAAAGCTGAA
gi|242 CCAAATGCTACCCATGACTACAACACGTCTTTCTCAAACCTCCAATGCTCACAAAGCTGAA
2930      2940      2950      2960      2970      2980
FIRST_      2560      2570      2580      2590      2600      2610
FIRST_ AAGAAGCTTCAAAACATTGATCACCCCTCTCACAAAGTCATCCAGTAAGAGAGATCACCGG
gi|242 AAGAAGCTTCAAAACATTGATCACCCCTCTCACAAAGTCATCCAGTAAGAGAGATCACCGG
2990      3000      3010      3020      3030      3040
FIRST_      2620      2630      2640      2650      2660      2670
FIRST_ CGTTCTGTTGATTCCAGAAATACCCCTCAATGATCTCCTGAAGCATCTGAATGACCCAAAT
gi|242 CGTTCTGTTGATTCCAGAAATACCCCTCAATGATCTCCTGAAGCATCTGAATGACCCAAAT
3050      3060      3070      3080      3090      3100
FIRST_      2680      2690      2700      2710      2720      2730
FIRST_ AGTAACCCCAAAGCCATCATGGGAGACATCCAGATGGCACACCAGAACTTAATGCTGGAT
gi|242 AGTAACCCCAAAGCCATCATGGGAGACATCCAGATGGCACACCAGAACTTAATGCTGGAT
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      3110      3120      3130      3140      3150      3160
FIRST_      2740      2750      2760      2770      2780      2790
FIRST_ CCCATGGGATCGATGTCTGAGGTCCCACCTAAAGTCCCTAACCGGGAGGCATCGCTATAC
      .....
gi|242 CCCATGGGATCGATGTCTGAGGTCCCACCTAAAGTCCCTAACCGGGAGGCATCGCTATAC
      3170      3180      3190      3200      3210      3220

      2800      2810      2820      2830      2840      2850
FIRST_ TCCCCCTCCTTCAACTCTCCCCAGAAATAGCCCAACCAAGCGAGTGGATGTCCCCACCACT
      .....
gi|242 TCCCCCTCCTTCAACTCTCCCCAGAAATAGCCCAACCAAGCGAGTGGATGTCCCCACCACT
      3230      3240      3250      3260      3270      3280

      2860      2870      2880      2890      2900      2910
FIRST_ CCTGGAGTCCCAATGACTTCTCTGGAAAGACAAAGAGGTATCACAAAAATTCCTCCCAG
      .....
gi|242 CCTGGAGTCCCAATGACTTCTCTGGAAAGACAAAGAGGTATCACAAAAATTCCTCCCAG
      3290      3300      3310      3320      3330      3340

      2920      2930      2940      2950      2960      2970
FIRST_ AGGCACCTCTATATCTGCTATGCCTAAAAACTTAAACTCACCAAATGGTGTTTTGTTATCC
      .....
gi|242 AGGCACCTCTATATCTGCTATGCCTAAAAACTTAAACTCACCAAATGGTGTTTTGTTATCC
      3350      3360      3370      3380      3390      3400

      2980      2990      3000      3010      3020      3030
FIRST_ AGACAGCCTAGTATGAACCGTGGAGGATATATGCCACCCCCACTGGGGCGAAGGTGGAC
      .....
gi|242 AGACAGCCTAGTATGAACCGTGGAGGATATATGCCACCCCCACTGGGGCGAAGGTGGAC
      3410      3420      3430      3440      3450      3460

      3040      3050      3060      3070      3080      3090
FIRST_ TATATTTCAGGGAACACCAGTGAGTGTTTCATCTGCAGCCTTCCCTCTCCAGACAGAGCAGC
      .....
gi|242 TATATTTCAGGGAACACCAGTGAGTGTTTCATCTGCAGCCTTCCCTCTCCAGACAGAGCAGC
      3470      3480      3490      3500      3510      3520

      3100      3110      3120      3130      3140      3150
FIRST_ TACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGACGCCGTCCTTAAAACCT
      .....
gi|242 TACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGACGCCGTCCTTAAAACCT
      3530      3540      3550      3560      3570      3580

      3160      3170      3180      3190      3200      3210
FIRST_ GACGTGCCACCAAAGCCTTCCTTTGTTTCCTCAAACCCCATCTGTCTAGACCACTGAACAAA
      .....
gi|242 GACGTGCCACCAAAGCCTTCCTTTGTTTCCTCAAACCCCATCTGTCTAGACCACTGAACAAA
      3590      3600      3610      3620      3630      3640

      3220
FIRST_ TACACATACTAG
      .....
gi|242 TACACATACTAGGCCTCAAGTGTGCTATTCCCATGTGGCTTTATCCTGTCCGTGTTGTTG
      3650      3660      3670      3680      3690      3700
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>>gi|24234740|ref|NM_153618.1| Homo sapiens sema domain, (6109 nt)
rev-comp initn: 71 init1: 71 opt: 76 Z-score: 42.0 bits: 23.6 E(): 0.79
banded Smith-Waterman score: 76; 75.000% identity (75.000% similar) in 32 nt overla
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      210      200      190      180      170      160
FIRST- ATATAAAGTGTGTCTCGAATTTTCAACATCAGCTGAAAGTCCAGCCTGTGCTGCGATTCA
      :: :: :::: : ::::: :::::
gi|242 CTTATGTGGTACCCAATGCCAGAATGTAAGAGTTGCAAGT-GATTTTGTGCTGCTATTCA
      4450      4460      4470      4480      4490      4500

      150      140      130      120      110      100
FIRST- TTGCCTGAAGGGCGTCCTCTAAAAACCGGATATTGCCTTGAATAGTGATAGTCGACAGTA
      ::
gi|242 TTAAAACTTGTATTCCAGTCTTGCCAGCTTAAGGAGATCAAGATATTAAGAGGTATCCTT
      4510      4520      4530      4540      4550      4560
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3222 residues in 1 query sequences

6109 residues in 1 library sequences

Scomplib [34t25]

start: Mon Nov 28 09:44:12 2005 done: Mon Nov 28 09:44:12 2005

Total Scan time: 0.030 Total Display time: 0.120

Function used was FASTA [version 3.4t25 Nov 12, 2004]